

SEQUENCE LISTING

<110> Takeda Pharmaceutical Company Limited

<120> A Novel Ligand For FPRL1 And Its Use

<130> G05-0027

<150> JP 2002-324189

<151> 2002-11-07

<150> JP 2002-367119

<151> 2002-12-18

<150> JP 2003-59073

<151> 2003-03-05

<150> JP 2003-191359

<151> 2003-07-03

<150> PCT/JP03/14138

<151> 2003-11-06

<160> 24

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<213> Human

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Leu Gly Val Thr Phe Val Leu Gly Val Leu Gly Asn Gly Leu Val Ile  
35 40 45  
Trp Val Ala Gly Phe Arg Met Thr Arg Thr Val Thr Thr Ile Cys Tyr  
50 55 60  
Leu Asn Leu Ala Leu Ala Asp Phe Ser Phe Thr Ala Thr Leu Pro Phe  
65 70 75 80  
Leu Ile Val Ser Met Ala Met Gly Glu Lys Trp Pro Phe Gly Trp Phe  
85 90 95  
Leu Cys Lys Leu Ile His Ile Val Val Asp Ile Asn Leu Phe Gly Ser  
100 105 110  
Val Phe Leu Ile Gly Phe Ile Ala Leu Asp Arg Cys Ile Cys Val Leu  
115 120 125  
His Pro Val Trp Ala Gln Asn His Arg Thr Val Ser Leu Ala Met Lys  
130 135 140  
Val Ile Val Gly Pro Trp Ile Leu Ala Leu Val Leu Thr Leu Pro Val  
145 150 155 160  
Phe Leu Phe Leu Thr Thr Val Thr Ile Pro Asn Gly Asp Thr Tyr Cys  
165 170 175  
Thr Phe Asn Phe Ala Ser Trp Gly Gly Thr Pro Glu Glu Arg Leu Lys  
180 185 190  
Val Ala Ile Thr Met Leu Thr Ala Arg Gly Ile Ile Arg Phe Val Ile  
195 200 205  
Gly Phe Ser Leu Pro Met Ser Ile Val Ala Ile Cys Tyr Gly Leu Ile  
210 215 220  
Ala Ala Lys Ile His Lys Lys Gly Met Ile Lys Ser Ser Arg Pro Leu  
225 230 235 240  
Arg Val Leu Thr Ala Val Val Ala Ser Phe Phe Ile Cys Trp Phe Pro  
245 250 255  
Phe Gln Leu Val Ala Leu Leu Gly Thr Val Trp Leu Lys Glu Met Leu

260	265	270
Phe Tyr Gly Lys Tyr Lys Ile Ile Asp Ile Leu Val Asn Pro Thr Ser		
275	280	285
Ser Leu Ala Phe Phe Asn Ser Cys Leu Asn Pro Met Leu Tyr Val Phe		
290	295	300
Val Gly Gln Asp Phe Arg Glu Arg Leu Ile His Ser Leu Pro Thr Ser		
305	310	315
Leu Glu Arg Ala Leu Ser Glu Asp Ser Ala Pro Thr Asn Asp Thr Ala		
325	330	335
Ala Asn Ser Ala Ser Pro Pro Ala Glu Thr Glu Leu Gln Ala Met		
340	345	350

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<211> 1053

<212> DNA

<213> Human

<400> 3

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gtcctgggca atgggcttgt gatctgggtg gctggattcc ggatgacacg cacagtcacc	180
accatctgtt acctgaacct ggccctggct gacttttctt tcacggccac attaccattc	240
ctcattgtct ccatggccat gggagaaaaa tggccttttg gctggttcct gtgtaagtta	300
attcacatcg tggtagacat caacctcttt ggaagtgtct tcttgattgg tticattgca	360
ctggaccgct gcatttgtgt cctgcatcca gtctgggccc agaaccaccg cactgtgagt	420
ctggccatga aggtgatcgt cggaccttgg attcttgctc tagtccttac ctigccagtt	480
ttctctttt tgactacagt aactattcca aatggggaca catactgtac tttcaacttt	540
gcatcctggg gtggcacccc tgaggagagg ctgaaggtgg ccattacat gctgacagcc	600
agagggatta tccggtttgt cattggcttt agcttgccga tgtccattgt tgccatctgc	660
tatgggctca ttgcagccaa gatccacaaa aagggcata ttaaattcag ccgtccctta	720
cgggtcctca ctgctgttgt ggcttctttt ttcattctgt ggtttccctt tcaactggtt	780
gcccttctgg gcaccgtctg gctcaaagag atgttgttct atggcaagta caaaatcatt	840
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<400> 4

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			20					25					30		
Leu	Ser	Ile	Thr	Phe	Val	Leu	Gly	Val	Leu	Gly	Asn	Gly	Leu	Val	Ile
			35					40					45		
Trp	Val	Ala	Gly	Phe	Arg	Met	Val	His	Thr	Val	Thr	Thr	Thr	Cys	Phe
			50					55					60		
Leu	Asn	Leu	Ala	Leu	Ala	Asp	Phe	Ser	Phe	Thr	Val	Thr	Leu	Pro	Phe
			65					70					75		80
Phe	Val	Ile	Ser	Ile	Ala	Met	Lys	Glu	Lys	Trp	Pro	Phe	Gly	Trp	Phe
								85					90		95
Leu	Cys	Lys	Leu	Val	His	Ile	Val	Val	Asp	Ile	Asn	Leu	Phe	Gly	Ser
								100					105		110
Val	Phe	Leu	Ile	Ala	Leu	Ile	Ala	Leu	Asp	Arg	Cys	Ile	Cys	Val	Leu
								115					120		125
His	Pro	Val	Trp	Ala	Gln	Asn	His	Arg	Thr	Val	Ser	Leu	Ala	Arg	Lys
								130					135		140
Val	Val	Val	Gly	Pro	Trp	Ile	Leu	Ala	Leu	Ile	Leu	Thr	Leu	Pro	Ile
								145					150		155
Phe	Ile	Phe	Met	Thr	Thr	Val	Arg	Ile	Pro	Gly	Gly	Asn	Val	Tyr	Cys
								165					170		175
Thr	Phe	Asn	Phe	Ala	Ser	Trp	Gly	Asn	Thr	Ala	Glu	Glu	Leu	Leu	Asn
								180					185		190
Ile	Ala	Asn	Thr	Phe	Val	Thr	Val	Arg	Gly	Ser	Ile	Arg	Phe	Ile	Ile
								195					200		205
Gly	Phe	Ile	Met	Pro	Met	Ser	Ile	Val	Ala	Ile	Cys	Tyr	Gly	Leu	Ile
								210					215		220
Ala	Val	Lys	Ile	His	Arg	Arg	Ala	Leu	Val	Asn	Ser	Ser	Arg	Pro	Leu

225	230	235	240
Arg Val Leu Thr Ala Val Val Ala Ser Phe Phe Ile Cys Trp Phe Pro			
	245	250	255
Phe Gln Leu Val Ala Leu Leu Gly Thr Ile Trp Phe Lys Glu Ser Leu			
	260	265	270
Phe Ser Gly Arg Tyr Lys Ile Leu Asp Met Trp Val His Pro Thr Ser			
	275	280	285
Ser Leu Ala Tyr Phe Asn Ser Cys Leu Asn Pro Met Leu Tyr Ala Phe			
	290	295	300
Met Gly Gln Asp Phe His Glu Arg Leu Ile His Ser Leu Pro Ser Ser			
305	310	315	320
Leu Glu Arg Ala Leu Ser Glu Asp Ser Gly Gln Thr Ser Asp Thr Gly			
	325	330	335
Ile Ser Ser Ala Leu Pro Pro Val Asn Ile Asp Ile Lys Ala Ile			
	340	345	350

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gtgctgggta atggactagt gatctgggta gctggattcc ggatgggtaca cactgtcacc	180
actacctgtt tctgaatct agctttggct gacttctctt tcacagtgc tctaccattc	240
tttgtcatct caattgctat gaaagaaaaa tggccttttg gatggttcct gtgtaaatta	300
gttcacattg tagtagacat aaacctcttt ggaagtgtct tcctgattgc ttttaattgcc	360
ttggaccgct gcatttgtgt cctgcatcca gtctgggctc agaaccaccg cactgtgagc	420
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tttatattca tgactacagt tagaatcct ggaggcaatg tgtactgtac attcaacttc	540
gcacctctgg gtaacactgc tgaagaacta ttgaacatag ctaacacttt tgtaacagtt	600
agaggagca tcaggttcat tattggcttc ataatgccta tgtccattgt tgccatctgc	660
tatggactca tcgctgtcaa gatccacaga agagcacttg ttaattccag ccgtccatta	720
agagtcccta cagcagttgt ggcttccttc tttatctgtt ggtttcctt tcaactgggtg	780
gcccttttag gtacaatctg gtttaaagag tcattgttta gtggtcgtta caaaattctt	840

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ctctatgctt tcatgggcca ggactttcat gaaagactga ttcattccct gccttcaggt 960  
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<213> Mouse

<400> 6

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Tyr Asp Ser Thr Ile Ser Arg Val Leu Trp Ile Leu Ser Met Val Val  
20 25 30  
Val Ser Ile Thr Phe Phe Leu Gly Val Leu Gly Asn Gly Leu Val Ile  
35 40 45  
Trp Val Ala Gly Phe Arg Met Pro His Thr Val Thr Thr Ile Trp Tyr  
50 55 60  
Leu Asn Leu Ala Leu Ala Asp Phe Ser Phe Thr Ala Thr Leu Pro Phe  
65 70 75 80  
Leu Leu Val Glu Met Ala Met Lys Glu Lys Trp Pro Phe Gly Trp Phe  
85 90 95  
Leu Cys Lys Leu Val His Ile Val Val Asp Val Asn Leu Phe Gly Ser  
100 105 110  
Val Phe Leu Ile Ala Leu Ile Ala Leu Asp Arg Cys Ile Cys Val Leu  
115 120 125  
His Pro Val Trp Ala Gln Asn His Arg Thr Val Ser Leu Ala Arg Lys  
130 135 140  
Val Val Val Gly Pro Trp Ile Phe Ala Leu Ile Leu Thr Leu Pro Ile  
145 150 155 160  
Phe Ile Phe Leu Thr Thr Val Arg Ile Pro Gly Gly Asp Val Tyr Cys  
165 170 175  
Thr Phe Asn Phe Gly Ser Trp Ala Gln Thr Asp Glu Glu Lys Leu Asn  
180 185 190  
Thr Ala Ile Thr Phe Val Thr Thr Arg Gly Ile Ile Arg Phe Leu Ile

195	200	205
Gly Phe Ser Met Pro Met Ser Ile Val Ala Val Cys Tyr Gly Leu Ile		
210	215	220
Ala Val Lys Ile Asn Arg Arg Asn Leu Val Asn Ser Ser Arg Pro Leu		
225	230	235
Arg Val Leu Thr Ala Val Val Ala Ser Phe Phe Ile Cys Trp Phe Pro		
	245	250
Phe Gln Leu Val Ala Leu Leu Gly Thr Val Trp Phe Lys Glu Thr Leu		
	260	265
Leu Ser Gly Ser Tyr Lys Ile Leu Asp Met Phe Val Asn Pro Thr Ser		
	275	280
Ser Leu Ala Tyr Phe Asn Ser Cys Leu Asn Pro Met Leu Tyr Val Phe		
	290	295
Met Gly Gln Asp Phe Arg Glu Arg Phe Ile His Ser Leu Pro Tyr Ser		
305	310	315
Leu Glu Arg Ala Leu Ser Glu Asp Ser Gly Gln Thr Ser Asp Ser Ser		
	325	330
Thr Ser Ser Thr Ser Pro Pro Ala Asp Ile Glu Leu Lys Ala Pro		
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		350

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<212> DNA

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<400> 7

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gtgctgggca atggactagt gatttgggta gctggattcc ggatgccaca cactgtcacc	180
actatctgggt atctgaatct agcattggct gacttttctt tcacagcaac tctaccattc	240
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gttcacattg tggtagatgt aaacctgttt ggaagtgtct tcttgattgc tctcattgcc	360
ttggaccgct gcatttgtgt tctgcatcca gtctgggctc agaaccaccg cactgtgagc	420
ctggctagga agtggttgtt tgggccctgg atttttgctc tgattctcac ttgcccatt	480
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cgagtcctta cagcagttgt ggcttccttc tttatctgct ggtttcctt tcagcttggtg 780
gcccttttgg gcacagtctg gtttaaagag acattgccta gtggtagtta taaaattctt 840
gacatgtttg ttaacccaac aagctcattg gcttacttca atagtgtct caatccgatg 900
ctctatgttt tcatgggcca ggactttcgt gagagattta ttcattccct gccttatagt 960
cttgagagag cctgagtgga ggattctggt caaaccagtg attcaagcac cagttctact 1020
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<213> Artificial Sequence

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<223> Primer

<400> 8

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<223> Primer

<400> 9

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ctttctagat catggggcct ttaactcaat gtc 33

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<210> 10

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<212> DNA

<213> Artificial Sequence



<220>

<223> Primer

<400> 10

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<210> 11

<211> 27

<212> DNA

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<223> Primer

<400> 11

tctttcatga aagtcctggc ccatgaa 27

<210> 12

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<212> DNA

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<223> Primer

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aggaattcta actgtagtca tgaa 24

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<223> Primer

<400> 13

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<210> 14

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<213> Artificial Sequence

<220>

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<211> 13

<212> PRT

<213> Human

<400> 16

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<211> 15

<212> PRT

<213> Porcine

<400> 17

Met Thr Asn Ile Arg Lys Ser His Pro Leu Met Lys Ile Ile Asn

1 5 10 15

<210> 18

<211> 16

<212> PRT

<213> Porcine

<400> 18

Met Thr Asn Ile Arg Lys Ser His Pro Leu Met Lys Ile Ile Asn Asn

1 5 10 15

<210> 19

<211> 15

<212> PRT

<213> Human

<400> 19

Met Thr Pro Met Arg Lys Ile Asn Pro Leu Met Lys Leu Ile Asn

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1 5 10 15

<210> 21

<211> 15

<212> PRT

<213> Porcine

<400> 21

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<210> 22

<211> 15

<212> PRT

<213> Human

<400> 22

Met Phe Ala Asp Arg Trp Leu Phe Ser Thr Asn His Lys Asp Ile  
1 5 10 15

<210> 23

<211> 18

<212> PRT

<213> Porcine

<400> 23

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1 5 10 15

<210> 24

<211> 18

<212> PRT

<213> Human

<400> 24

Met Thr Pro Met Arg Lys Ile Asn Pro Leu Met Lys Leu Ile Asn His Ser Phe  
1 5 10 15